

CRF Errors Corrected by the STIC Systems Branch

1602

1/29/2003

Serial Number: 09/515,806A

CRF Processing Date:

Edited by:

Verified by:

(STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



1600

RAW SEQUENCE LISTING

DATE: 01/29/2003

PATENT APPLICATION: US/09/515,806A

TIME: 08:33:45

Input Set : N:\CrF4\01242003\I515806A.raw

Output Set: N:\CRF4\01292003\I515806A.raw

C--> 1 <110> APPLICANT: MILLENNIUM PHARMACEUTICALS, INC.
 2 Cook, William
 3 Kapeller-Libermann, Rosana
 4 <120> TITLE OF INVENTION: 14790, NOVEL PROTEIN KINASE MOLECULE AND
 5 USES TREREFOR
 6 <130> FILE REFERENCE: 38155-20002.00
 7 <140> CURRENT APPLICATION NUMBER: US/09/515,806A
 8 <141> CURRENT FILING DATE: 2000-02-29
 9 <160> NUMBER OF SEQ ID NOS: 33
 10 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 5525
 14 <212> TYPE: DNA
 15 <213> ORGANISM: Homo sapiens
 16 <220> FEATURE:
 17 <221> NAME/KEY: CDS
 18 <222> LOCATION: (63)...(5012)
 19 <400> SEQUENCE: 1

20 tcgccccacg cgtccgcacc gccgcccagg caaggccgcc ctgccttggg cgcagcgcgtg 60
 21 cc atg gct ggg ggc cgt ggg gcc ccc ggg cgc ggc cgg gac gag cct 107
 22 Met Ala Gly Gly Arg Gly Ala Pro Gly Arg Gly Arg Asp Glu Pro
 23 1 5 10 15
 24 ccg gag agc tac ccg caa cga cag gac cac gag cta cag gcc ctg gag 155
 25 Pro Glu Ser Tyr Pro Gln Arg Gln Asp His Glu Leu Gln Ala Leu Glu
 26 20 25 30
 27 gcc atc tac ggc gcg gac ttc caa gac ctg cgg ccg gac gct tgc gga 203
 28 Ala Ile Tyr Gly Ala Asp Phe Gln Asp Leu Arg Pro Asp Ala Cys Gly
 29 35 40 45
 30 ccg gtc aaa gag ccc cct gaa atc aat tta gtt ttg tac cct caa ggc 251
 31 Pro Val Lys Glu Pro Pro Glu Ile Asn Leu Val Leu Tyr Pro Gln Gly
 32 50 55 60
 33 cta act ggt gaa gaa gta tat gta aaa gtg gat ttg agg gtt aaa tgc 299
 34 Leu Thr Gly Glu Glu Val Tyr Val Lys Val Asp Leu Arg Val Lys Cys
 35 65 70 75
 36 cca cct acc tat cca gat gta gtt cct gaa ata gag tta aaa aat gcc 347
 37 Pro Pro Thr Tyr Pro Asp Val Val Pro Glu Ile Glu Leu Lys Asn Ala
 38 80 85 90 95
 39 aaa ggt cta tca aat gaa agt gtc aat ttg tta aaa tct cgc cta gaa 395
 40 Lys Gly Leu Ser Asn Glu Ser Val Asn Leu Leu Lys Ser Arg Leu Glu
 41 100 105 110
 42 gaa ctg gcc aag aaa cac tgt ggg gag gtg atg atc ttt gaa ctg gct 443
 43 Glu Leu Ala Lys Lys His Cys Gly Glu Val Met Ile Phe Glu Leu Ala
 44 115 120 125

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Input Set : N:\CrF4\01242003\I515806A.raw

Output Set: N:\CRF4\01292003\I515806A.raw

45	tac cac gtg cag tca ttt ctc agc gag cat aac aag ccc cct ccc aag	491
46	Tyr His Val Gln Ser Phe Leu Ser Glu His Asn Lys Pro Pro Pro Lys	
47	130 135 140	
48	tct ttt cat gaa gaa atg ctg gaa agg cgg gct cag gag gag cag cag	539
49	Ser Phe His Glu Glu Met Leu Glu Arg Arg Ala Gln Glu Glu Gln Gln	
50	145 150 155	
51	agg ctg ttg gag gcc aag cgg aaa gaa gag cag gag caa cgt gaa atc	587
52	Arg Leu Leu Glu Ala Lys Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile	
53	160 165 170 175	
54	ctg cat gag att cag aga agg aaa gaa gag ata aaa gaa gag aaa aaa	635
55	Leu His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys	
56	180 185 190	
57	agg aaa gaa atg gct aag cag gaa cgt ttg gaa att gct agt ttg tca	683
58	Arg Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Ala Ser Leu Ser	
59	195 200 205	
60	aac caa gat cat acc tct aag aag gac cca gga gga cac aga acg gct	731
61	Asn Gln Asp His Thr Ser Lys Lys Asp Pro Gly Gly His Arg Thr Ala	
62	210 215 220	
63	gcc att cta cat gga ggc tct cct gac ttt gta gga aat ggt aaa cat	779
64	Ala Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys His	
65	225 230 235	
66	cgg gca aac tcc tca gga agg tct agg cga gaa cgt cag tat tct gta	827
67	Arg Ala Asn Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val	
68	240 245 250 255	
69	tgt aat agt gaa gat tct cct ggc tct tgt gaa att ctg tat ttc aat	875
70	Cys Asn Ser Glu Asp Ser Pro Gly Ser Cys Glu Ile Leu Tyr Phe Asn	
71	260 265 270	
72	atg ggg agt cct gat cag ctc atg gtg cac aaa ggg aaa tgt att ggc	923
73	Met Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Lys Cys Ile Gly	
74	275 280 285	
75	agt gat gaa caa ctt gga aaa tta gtc tac aat gct ttg gaa aca gcc	971
76	Ser Asp Glu Gln Leu Gly Lys Leu Val Tyr Asn Ala Leu Glu Thr Ala	
77	290 295 300	
78	act ggt ggc ttt gtc ttg ttg tat gag tgg gtc ctt cag tgg cag aaa	1019
79	Thr Gly Gly Phe Val Leu Leu Tyr Glu Trp Val Leu Gln Trp Gln Lys	
80	305 310 315	
81	aaa atg ggt cca ttc ctt acc agt caa gaa aaa gag aag att gat aag	1067
82	Lys Met Gly Pro Phe Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys	
83	320 325 330 335	
84	tgc aaa aag cag att caa gga aca gaa aca gaa ttc aac tca ctg gta	1115
85	Cys Lys Lys Gln Ile Gln Gly Thr Glu Thr Glu Phe Asn Ser Leu Val	
86	340 345 350	
87	aaa ttg agc cat cca aat gta gta cgc tac ctt gca atg aat ctc aaa	1163
88	Lys Leu Ser His Pro Asn Val Val Arg Tyr Leu Ala Met Asn Leu Lys	
89	355 360 365	
90	gag caa gac gac tcc atc gtg gtg gac att tta gtg gag cac att agt	1211
91	Glu Gln Asp Asp Ser Ile Val Val Asp Ile Leu Val Glu His Ile Ser	
92	370 375 380	
93	ggg gtc tct ctt gct gca cac ctg agc cac tca ggc ccc atc cct gtg	1259

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Input Set : N:\CrF4\01242003\I515806A.raw

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94	Gly Val Ser Leu Ala Ala His Leu Ser His Ser Gly Pro Ile Pro Val	
95	385 390 395	
96	cat cag ctt cgc agg tac aca gct cag ctc ctg tca ggc ctt gat tat	1307
97	His Gln Leu Arg Arg Tyr Thr Ala Gln Leu Leu Ser Gly Leu Asp Tyr	
98	400 405 410 415	
99	ctg cac agc aat tct gtg gtg cat aag gtc ctg agt gca tct aat gtc	1355
100	Leu His Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Asn Val	
101	420 425 430	
102	ttg gtg gat gca gaa ggc acc gtc aag att acg gac tat agc att tct	1403
103	Leu Val Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser	
104	435 440 445	
105	aag cgc ctc gca gac att tgc aag gag gat gtg ttt gag caa acc cga	1451
106	Lys Arg Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Thr Arg	
107	450 455 460	
108	gtt cgt ttt agt gac aat gct ctg cct tat aaa acg ggg aag aaa gga	1499
109	Val Arg Phe Ser Asp Asn Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly	
110	465 470 475	
111	gat gtt tgg cgt ctt ggc ctt ctg ctg ctg tcc ctc agc caa gga cag	1547
112	Asp Val Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln	
113	480 485 490 495	
114	gaa tgt gga gag tac cct gtg acc atc cct agt gac tta cca gct gac	1595
115	Glu Cys Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp	
116	500 505 510	
117	ttt caa gat ttt cta aag aaa tgt gtg tgc ttg gat gac aag gaa aga	1643
118	Phe Gln Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg	
119	515 520 525	
120	tgg agt ccc cag cag ttg ttg aaa cac agc ttt ata aat ccc cag cca	1691
121	Trp Ser Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro	
122	530 535 540	
123	aaa atg cct cta gtg gaa caa agt cct gaa gat tct gga gga caa gat	1739
124	Lys Met Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp	
125	545 550 555	
126	tat gtt gag act gtt att cct agc aac cgg cta ccc agt gct gcc ttc	1787
127	Tyr Val Glu Thr Val Ile Pro Ser Asn Arg Leu Pro Ser Ala Ala Phe	
128	560 565 570 575	
129	ttt agt gag aca cag aga cag ttt tcc cga tac ttc att gag ttt gaa	1835
130	Phe Ser Glu Thr Gln Arg Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu	
131	580 585 590	
132	gaa tta caa ctt ctt ggt aaa gga gct ttt gga gct gtc atc aag gtg	1883
133	Glu Leu Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val	
134	595 600 605	
135	cag aac aag ttg gac ggc tgc tgc tac gca gtg aag cgc atc ccc atc	1931
136	Gln Asn Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile	
137	610 615 620	
138	aac ccg gcc agc cgg cag ttc cgc agg atc aag ggc gaa gtg aca ctg	1979
139	Asn Pro Ala Ser Arg Gln Phe Arg Arg Ile Lys Gly Glu Val Thr Leu	
140	625 630 635	
141	ctg tca cgg ctg cac cat gag aac att gtg cgc tac tac aac gcc tgg	2027
142	Leu Ser Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp	

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Input Set : N:\CrF4\01242003\I515806A.raw

Output Set: N:\CRF4\01292003\I515806A.raw

143	640	645	650	655	
144	atc gag cgg cac gag cgg ccg gcg gga ccg ggg acg ccg ccc ccg gac				2075
145	Ile Glu Arg His Glu Arg Pro Ala Gly Pro Gly Thr Pro Pro Pro Asp				
146		660	665	670	
147	tcc ggg ccc ctg gcc aag gat gac cga gct gca cgc ggg cag ccg gcg				2123
148	Ser Gly Pro Leu Ala Lys Asp Asp Arg Ala Ala Arg Gly Gln Pro Ala				
149		675	680	685	
150	agc gac aca gac ggc ctg gac agc gta gag gcc gcc gcg ccg cca ccc				2171
151	Ser Asp Thr Asp Gly Leu Asp Ser Val Glu Ala Ala Pro Pro Pro				
152		690	695	700	
153	atc ctc agc agc tcg gtg gag tgg agc act tcg ggc gag cgc tcg gcc				2219
154	Ile Leu Ser Ser Ser Val Glu Trp Ser Thr Ser Gly Glu Arg Ser Ala				
155		705	710	715	
156	agt gcc cgt ttc ccc gcc acc ggc ccg ggc tcc agc gat gac gag gac				2267
157	Ser Ala Arg Phe Pro Ala Thr Gly Pro Gly Ser Ser Asp Asp Glu Asp				
158		720	725	730	735
159	gac gac gag gac gag cac ggt ggc gtc ttc tcc cag tcc ttc ctg cct				2315
160	Asp Asp Glu Asp Glu His Gly Gly Val Phe Ser Gln Ser Phe Leu Pro				
161		740	745	750	
162	gct tca gat tct gaa agt gat att atc ttt gac aat gaa gat gag aac				2363
163	Ala Ser Asp Ser Glu Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn				
164		755	760	765	
165	agt aaa agt cag aat cag gat gaa gat tgc aat gaa aag aat ggc tgc				2411
166	Ser Lys Ser Gln Asn Gln Asp Glu Asp Cys Asn Glu Lys Asn Gly Cys				
167		770	775	780	
168	cat gaa agt gag cca tca gtg acg act gag gct gtg cac tac cta tac				2459
169	His Glu Ser Glu Pro Ser Val Thr Thr Glu Ala Val His Tyr Leu Tyr				
170		785	790	795	
171	atc cag atg gag tac tgt gag aag agc act tta cga gac acc att gac				2507
172	Ile Gln Met Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp				
173		800	805	810	815
174	cag gga ctg tat cga gac acc gtc aga ctc tgg agg ctt ttt cga gag				2555
175	Gln Gly Leu Tyr Arg Asp Thr Val Arg Leu Trp Arg Leu Phe Arg Glu				
176		820	825	830	
177	att ctg gat gga tta gct tat atc cat gag aaa gga atg att cac ccg				2603
178	Ile Leu Asp Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg				
179		835	840	845	
180	gat ttg aag cct gtc aac att ttt ttg gat tct gat gac cat gtg aaa				2651
181	Asp Leu Lys Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys				
182		850	855	860	
183	ata ggt gat ttt ggt ttg gcg aca gac cat cta gcc ttt tct gct gac				2699
184	Ile Gly Asp Phe Gly Leu Ala Thr Asp His Leu Ala Phe Ser Ala Asp				
185		865	870	875	
186	agc aaa caa gac gat cag aca gga gac ttg att aag tca gac cct tca				2747
187	Ser Lys Gln Asp Asp Gln Thr Gly Asp Leu Ile Lys Ser Asp Pro Ser				
188		880	885	890	895
189	ggt cac tta act ggg atg gtt ggc act gct ctc tat gta agc cca gag				2795
190	Gly His Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu				
191		900	905	910	

RAW SEQUENCE LISTING

DATE: 01/29/2003

PATENT APPLICATION: US/09/515,806A

TIME: 08:33:45

Input Set : N:\Crf4\01242003\I515806A.raw

Output Set: N:\CRF4\01292003\I515806A.raw

192	gtc caa gga agc acc aaa tct gca tac aac cag aaa gtg gat ctc ttc	2843
193	Val Gln Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe	
194	915 920 925	
195	agc ctg gga att atc ttc ttt gag atg tcc tat cac ccc atg gtc acg	2891
196	Ser Leu Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr	
197	930 935 940	
198	gct tca gaa agg atc ttt gtt ctc aac caa ctc aga gat ccc act tcg	2939
199	Ala Ser Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser	
200	945 950 955	
201	cct aag ttt cca gaa gac ttt gag gat gga gag cat gca aag cag aaa	2987
202	Pro Lys Phe Pro Glu Asp Phe Asp Asp Gly Glu His Ala Lys Gln Lys	
203	960 965 970 975	
204	tca gtc atc tcc tgg ctg ttg aac cac gat cca gca aaa cgg ccc aca	3035
205	Ser Val Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr	
206	980 985 990	
207	gcc aca gaa ctg ctc aag agt gag ctg ctg ccc cca ccc cag atg gag	3083
208	Ala Thr Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu	
209	995 1000 1005	
210	gag tca gag ctg cat gaa gtg ctg cac cac acg ctg acc aac gtg gat	3131
211	Glu Ser Glu Leu His Glu Val Leu His His Thr Leu Thr Asn Val Asp	
212	1010 1015 1020	
213	ggg aag gcc tac cgc acc atg atg gcc cag atc ttc tcg cag cgc atc	3179
214	Gly Lys Ala Tyr Arg Thr Met Met Ala Gln Ile Phe Ser Gln Arg Ile	
215	1025 1030 1035	
216	tcc cct gcc atc gat tac acc tat gac agc gac ata ctg aag ggc aac	3227
217	Ser Pro Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn	
218	1040 1045 1050 1055	
219	ttc tca atc cgt aca gcc aag atg cag cag cat gtg tgt gaa acc atc	3275
220	Phe Ser Ile Arg Thr Ala Lys Met Gln Gln His Val Cys Glu Thr Ile	
221	1060 1065 1070	
222	atc cgc atc ttt aaa aga cat gga gct gtt cag ttg tgt act cca cta	3323
223	Ile Arg Ile Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu	
224	1075 1080 1085	
225	ctg ctt ccc cga aac aga caa ata tat gag cac aac gaa gct gcc cta	3371
226	Leu Leu Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu	
227	1090 1095 1100	
228	ttc atg gac cac agc ggg atg ctg gtg atg ctt cct ttt gac ctg cgg	3419
229	Phe Met Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg	
230	1105 1110 1115	
231	atc cct ttt gca aga tat gtg gca aga aat aat ata ttg aat tta aaa	3467
232	Ile Pro Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys	
233	1120 1125 1130 1135	
234	cga tac tgc ata gaa cgt gtg ttc agg ccg cgc aag tta gat cga ttt	3515
235	Arg Tyr Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe	
236	1140 1145 1150	
237	cat ccc aaa gaa ctt ctg gag tgt gca ttt gat att gtc act tct acc	3563
238	His Pro Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr	
239	1155 1160 1165	
240	acc aac agc ttt ctg ccc act gct gaa att atc tac act atc tat gaa	3611

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/515,806A

DATE: 01/29/2003
TIME: 08:33:46

Input Set : N:\Crf4\01242003\I515806A.raw
Output Set: N:\CRF4\01292003\I515806A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 1,2,3,4,5,6,7,8,9,11,13,14,15,16,18,19,20,21,22,23,24,25
Seq#:6; Xaa Pos. 26,27,28,29,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45
Seq#:6; Xaa Pos. 46,47,48,49,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65
Seq#:6; Xaa Pos. 66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84
Seq#:6; Xaa Pos. 85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102
Seq#:6; Xaa Pos. 103,104,105,106,107,108,109,110,111,112,113,114,115,116
Seq#:6; Xaa Pos. 118,119,120,121,122,123,124,125,129,131,132,134,135,136
Seq#:6; Xaa Pos. 137,138,139,140,141,142,143,144,145,146,147,148,149,150
Seq#:6; Xaa Pos. 152,153,157,158,159,160,161,162,163,164,165,166,167,168
Seq#:6; Xaa Pos. 169,170,171,172,173,174,175,176,177,179,180,181,182,183
Seq#:6; Xaa Pos. 184,185,186,187,188,189,190,191,193,194,195,197,198,199
Seq#:6; Xaa Pos. 200,201,202,203,204,205,206,207,208,209,210,211,212,213
Seq#:6; Xaa Pos. 214,215,216,217,218,219,220,221,222,223,224,225,226,227
Seq#:6; Xaa Pos. 228,229,230,231,232,233,234,235,236,237,238,239,240,241
Seq#:6; Xaa Pos. 242,243,244,245,246,247,248,249,250,251,253,254,255,256
Seq#:6; Xaa Pos. 257,258,259,260,261,262,263,264,265,266,268,269,270
Seq#:7; Xaa Pos. 2,4,5,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24
Seq#:7; Xaa Pos. 25,26,27,28,29